

Sequence Listing

SEQ ID NO: 1

	GGCACGAGGCTTCTGGCCAGGGAACGTGGAAGGCGCACCGACAGGGATCCGGCCAGGGAG	60
5	GGCGAGTGAAAGAAGGAAATCAGAAAGGAAGGGAGTTAACAAAATAATAAAAAACAGCCTG	120
	AGCCACGGCTGGAGAGACCGAGACCCGGCGCAAGAGAGCGCAGCCTTAGTAGGAGAGGAA	180
	CGCGAGACGCGGCAGCGCAGAGCGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	240
	AGGCGCCGCAGCTGAGACCGGCGGCCGACGGCCAGCCCTCAGGGGGCGGTACAAGTCAG	300
	CGCCCAAGCAAGTCAAGCGACAGCGCTCGTCTTCGCCCCAACTGATGCGCTGCAAACGCC	360
10	GGCTCAACTTCAGCGGCTTTGGCTACAGCCTGCCGCAGCAGCAGCCGGCCGCCGTGGCGC	420
	GCCGCAACGAGCGCGAGCGCAACCGCGTCAAGTTGGTCAACCTGGGCTTTGCCACCCTTC	480
	GGGAGCACGTCCCCAACGGCGCGGCCAACAAGAAGATGAGTAAGGTGGAGACACTGCGCT	540
	CGGCGGTGAGTACATCCGCGCGCTGCAGCAGCTGCTGGACGAGCATGACGCGGTGAGCG	600
	CCGCCTTCCAGGCAGGCGTCCTGTGCCCCACCATCTCCCCAACTACTCCAACGACTTGA	660
15	ACTCCATGGCCGGCTCGCCGGTCTCATCCTACTCGTCGGACGAGGGCTCTTACGACCCGC	720
	TCAGCCCCGAGGAGCAGGAGCTTCTCGACTTCACCAACTGGTTCTGAGGGGCTCGGCCTG	780
	GTCAGGCCCTGGTGCGAATGGACTTTGGAAGCAGGGTGATCGCACAACTGCATCTTTAG	840
	TGCTTCTTGTGTCAGTGGCGTTGGGAGGGGGAGAAAAGGAAAAGAAAAAAGAAGAAGA	900
	AGAAGAAAAGAGAAGAAGAAAAAACGAAAACAGTCAACCAACCCCATCGCCAACTAAGC	960
20	GAGGCATGCCTGAGAGACATGGCTTTCAGAAAACGGGAAGCGCTCAGAACAGTATCTTTG	1020
	CACTCCAATCATTACGGAGATATGAAGAGCAACTGGGACCTGAGTCAATGCGCAAAATG	1080
	CAGCTTGTGTGCAAAAGCAGTGGGCTCCTGGCAGAAGGGAGCAGCACACGCGTTATAGTA	1140
	ACTCCCATCACCTCTAACACGCACAGCTGAAAGTTCTTGCTCGGGTCCCTTCACCTCCCC	1200
	GCCCTTTCTTAGAGTGCAGTTCCTTAGCCCTCTAGAAACGAGTTGGTGTCTTTCGTCTCAG	1260
25	TAGCCCCACCCCAATAAGCTGTAGACATTGGTTTACAGTGAACTATGCTATTCTCAGC	1320
	CCTTTGAAACTCTGCTTCTCCTCCAGGGCCCGATTCCCAAACCCCATGGCTTCCCTCACA	1380
	CTGTCTTTTCTACCATTTTTCATTATAGAATGCTTCCAATCTTTTGTGAATTTTTTATTAT	1440
	AAAAATCTATTTGTATCTATCCTAACAGTTCGGGGATATATTAAGATATTTTTGTACA	1500
	TAAGAGAGAAAGAGAGAGAAAAATTTATAGAAGTTTGTACAAATGGTTTAAATGTGTA	1560
30	TATCTTGATACTTTAACATGTAATGCTATTACCTCTGCATATTTTAGATGTGTAGTTCAC	1620
	CTTACAACCTGCAATTTTCCCTATGTGGTTTTGTAAAGAACTCTCCTCATAGGTGAGATCA	1680
	AGAGGCCACCAGTTGTACTTCAGCACCAATGTGTCTTACTTTATAGAAATGTTGTTAATG	1740
	TATTAATGATGTTATTAAATACTGTTCAAGAAGAACAAAGTTTATGCAGCTACTGTCCAA	1800
	ACTCAAAGTGGCAGCCAGTTGGTTTTGATAGGTTGCCTTTTGGAGATTCTATTACTGCC	1860
35	TTTTTTTTTCTTACTGTTTTATTACAACTTACAAAAATATGTATAACCCTGTTTTATACA	1920
	AACTAGTTTCGTAATAAACTTTTTTCCTTTTTTTTAAATG	1960

SEQ ID NO: 2

	Met	Arg	Cys	Lys	Arg	Arg	Leu	Asn	Phe	Ser	10
5	Gly	Phe	Gly	Tyr	Ser	Leu	Pro	Gln	Gln	Gln	20
	Pro	Ala	Ala	Val	Ala	Arg	Arg	Asn	Glu	Arg	30
	Glu	Arg	Asn	Arg	Val	Lys	Leu	Val	Asn	Leu	40
	Gly	Phe	Ala	Thr	Leu	Arg	Glu	His	Val	Pro	50
	Asn	Gly	Ala	Ala	Asn	Lys	Lys	Met	Ser	Lys	60
10	Val	Glu	Thr	Leu	Arg	Ser	Ala	Val	Glu	Tyr	70
	Ile	Arg	Ala	Leu	Gln	Gln	Leu	Leu	Asp	Glu	80
	His	Asp	Ala	Val	Ser	Ala	Ala	Phe	Gln	Ala	90
	Gly	Val	Leu	Ser	Pro	Thr	Ile	Ser	Pro	Asn	100
	Tyr	Ser	Asn	Asp	Leu	Asn	Ser	Met	Ala	Gly	110
15	Ser	Pro	Val	Ser	Ser	Tyr	Ser	Ser	Asp	Glu	120
	Gly	Ser	Tyr	Asp	Pro	Leu	Ser	Pro	Glu	Glu	130
	Gln	Glu	Leu	Leu	Asp	Phe	Thr	Asn	Trp	Phe	140

SEQ ID NO: 3

GGCACGAGGCTTCTGGCCAGGGAACGTGGAAGGCGCACCGACAGGGATCCGGCCAGGGAG 60
GGCGAGTGAAAGAAGGAAATCAGAAAGGAAGGGAGTTAACAAAATAATAAAAACAGCCTG 120
AGCCACGGCTGGAGAGACCGAGACCCGGCGCAAGAGAGCGCAGCCTTAGTAGGAGAGGAA 180
5 CGCGAGACGCGGCAGAGCGCGTTTCAGCACTGACTTTTGCTGCTGCTTCTGCTTTTTTTTTT 240
TCTTAGAAACAAGAAGGCGCCAGCGGCAGCCTCACACGCGAGCGCCACGCGAGGCTCCCCG 300
AAGCCAACCCGCGAAGGGAGGAGGGGAGGGAGGAGGAGGCGGCGTGCAGGGAGGAGAAAA 360
AGCATTTTTCACTTTTTTTTGCTCCCACTCTAAGAAGTCTCCCGGGGATTTTGTATATATTT 420
TTTAACTTCCGTCAGGGCTCCCGCTTCATATTTCCCTTTCTTTCCCTCTCTGTTCTCTGCA 480
10 CCCAAGTTGGTCAACCTGGGCTTTGCCACCCTTCGGGAGCACGTCCCCAACGGCGCGGCC 540
AACAGAAGATGAGTAAGGTGGAGACACTGCGCTCGGCGGTTCGAGTACATCCGCGCGCTG 600
CAGCAGCTGCTGGACGAGCATGACGCGGTGAGCGCCGCTTCCAGGCAGGCGTCCTGTCTG 660
CCCACCATCTCCCCCACTACTCCAACGACTTGAATCCATGGCCGGCTCGCCGGTCTCA 720
TCCTACTCGTCGGACGAGGGCTCTTACGACCCGCTCAGCCCCGAGGAGCAGGAGCTTCTC 780
15 GACTTCACCAACTGGTTCTGAGGGGCTCGGCCTGGTCAGGCCCTGGTGCGAATGGACTTT 840
GGAAGCAGGGTGATCGCACAACCTGCATCTTTAGTGCTTTCTTGTCAGTGGCGTTGGGAG 900
GGGGAGAAAAGGAAAAGAAAAAAAAAAGAAGAAGAAGAAGAAAAGAGAAGAAGAAAAAAC 960
GAAAACAGTCAACCAACCCCATCGCCAATAAGCGAGGCATGCCTGAGAGACATGGCTTT 1020
CAGAAAACGGGAAGCGCTCAGAACAGTATCTTTGCACTCCAATCATTACGGAGATATGA 1080
20 AGAGCAACTGGGACCTGAGTCAATGCGCAAAATGCAGCTTGTGTGCAAAAGCAGTGGGCT 1140
CCTGGCAGAAGGGAGCAGCACACGCGTTATAGTAACTCCCATCACCTCTAACACGCACAG 1200
CTGAAAGTTCTTGCTCGGGTCCCTTCACCTCCCCGCCCTTTCTTAGAGTGCAGTTCTTAG 1260
CCCTCTAGAAACGAGTTGGTGTCTTTCGTCTCAGTAGCCCCCACCCCAATAAGCTGTAGA 1320
CATTGGTTTACAGTGAACTATGCTATTCTCAGCCCTTTGAAACTCTGCTTCTCCTCCAG 1380
25 GGCCCGATTCCCAAACCCCATGGCTTCCCTCACACTGTCTTTTCTACCATTTTTCATTATA 1440
GAATGCTTCCAATCTTTTGTGAATTTTTTATTATAAAAAATCTATTTGTATCTATCCTAA 1500
CCAGTTCGGGGATATATTAAGATATTTTTGTACATAAGAGAGAAAGAGAGAGAAAAATTT 1560
ATAGAAGTTTTGTACAAATGGTTTTAAATGTGTATATCTTGATACTTTAACATGTAATGC 1620
TATTACCTCTGCATATTTTAGATGTGTAGTTCACCTTACAACCTGCAATTTTCCCTATGTG 1680
30 GTTTTGTAAAGAACTCTCCTCATAGGTGAGATCAAGAGGCCACCAGTTGTACTTCAGCAC 1740
CAATGTGTCTTACTTTATAGAAATGTTGTTAATGTATTAATGATGTTATTAAATACTGTT 1800
CAAGAAGAACAAAGTTTATGCAGCTACTGTCCAACTCAAAGTGGCAGCCAGTTGGTTTTT 1860
GATAGGTTGCCTTTTGGAGATTTCTATTACTGCCTTTTTTTTTCTTACTGTTTTATTACAA 1920
ACTTACAAAAATATGTATAACCCTGTTTTATACAACTAGTTTCGTAATAAACTTTTTTC 1980
35 CTTTTTTTAAATG 1994

SEQ ID NO: 4

	Met	Ser	Lys	Val	Glu	Thr	Leu	Arg	Ser	Ala	10
	Val	Glu	Tyr	Ile	Arg	Ala	Leu	Gln	Gln	Leu	20
	Leu	Asp	Glu	His	Asp	Ala	Val	Ser	Ala	Ala	30
5	Phe	Gln	Ala	Gly	Val	Leu	Ser	Pro	Thr	Ile	40
	Ser	Pro	Asn	Tyr	Ser	Asn	Asp	Leu	Asn	Ser	50
	Met	Ala	Gly	Ser	Pro	Val	Ser	Ser	Tyr	Ser	60
	Ser	Asp	Glu	Gly	Ser	Tyr	Asp	Pro	Leu	Ser	70
	Pro	Glu	Glu	Gln	Glu	Leu	Leu	Asp	Phe	Thr	80
10	Asn	Trp	Phe								83

SEQ ID NO: 5

GGCACGAGGCTTCTGGCCAGGGAACGTGGAAGGCGCACCGACAGGGATCCGGCCAGGGAG 60
GGCGAGTGAAAGAAGGAAATCAGAAAGGAAGGGAGTTAACAAAATAATAAAAACAGCCTG 120
AGCCACGGCTGGAGAGACCGAGACCCGGCGCAAGAGAGCGCAGCCTTAGTAGGAGAGGAA 180
5 CGCGAGACGCGGCAGAGCGCGTTTCACTGACTTTTGCTGCTGCTTCTGCTTTTTTTTTT 240
TCTTAGAAACAAGAAGGCGCCAGCGGCAGCCTCACACGCGAGCGCCACGCGAGGCTCCCCG 300
AAGCCAACCCGCGAAGGGAGGAGGGGAGGGAGGAGGAGGCGGCGTGCAGGGAGGAGAAAA 360
AGCATTTTCACTTTTTTTTGTCTCCCACTCTAAGAAGTCTCCCGGGGATTTTGTATATATTT 420
TTTAACTTCCGTCAGGGCTCCCGCTTCATATTTCTTTTCTTTCCCTCTCTGTTCTCTGCA 480
10 CCCAAGTTCTCTCTGTGTCCCCCTCGCGGGCCCCGCACCTCGCGTCCCGGATCGCTCTGA 540
TTCCGCGACTCCTTGGCCGCCGCTGCGCATGGAAAGCTCTGCCAAGATGGAGAGCGGCGG 600
CGCCGGCCAGCAGCCCCAGCCGCAGCCCCAGCAGCCCTTCCCTGCCGCCCGCAGCCTGTTT 660
CTTTGCCACGGCCGCAGCCGCGGCGGCCGCAGCCGCCGCAGCGGCAGCGCAGAGCGCGCA 720
GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGCGCCGCAGCTGAGACCGGCGGCCGA 780
15 CGGCCAGCCCTCAGGGGGCGGTACAAAGTCAGCGCCCCAAGCAAGTCAAGCGACAGCGCTC 840
GTCTTCGCCCCGAAGTATGCGCTGCAAACGCCGGCTCAACTTCAGCGGCTTTGGCTACAG 900
CCTGCCGCAGCAGCAGCTGCTGGACGAGCATGACGCGGTGAGCGCCGCTTCCAGGCAGG 960
CGTCTGTGCGCCACCATCTCCCCCACTACTCCAACGACTTGAAGTCCATGGCCGGCTC 1020
GCCGGTCTCATCCTACTCGTCGGACGAGGGCTCTTACGACCCGCTCAGCCCCGAGGAGCA 1080
20 GGAGCTTCTCGACTTCACCAACTGGTTCTGAGGGGCTCGGCCTGGTCAGGCCCTGGTGCG 1140
AATGGACTTTGGAAGCAGGGTGATCGCACAACTGCATCTTTAGTGCTTTCTTGTCAGTG 1200
GCGTTGGGAGGGGGAGAAAAGGAAAAGAAAAAAGAAGAAGAAGAAAAGAGAAGA 1260
AGAAAAAACGAAAACAGTCAACCAACCCCATCGCCAACTAAGCGAGGCATGCCTGAGAG 1320
ACATGGCTTTTCAGAAAACGGGAAGCGCTCAGAACAGTATCTTTGCACTCCAATCATTCAC 1380
25 GGAGATATGAAGAGCAACTGGGACCTGAGTCAATGCGCAAAATGCAGCTTGTGTGCAAAA 1440
GCAGTGGGCTCCTGGCAGAAGGGAGCAGCACACGCGTTATAGTAAGTCCCATCACCTCTA 1500
ACACGCACAGCTGAAAGTTCTTGCTCGGGTCCCTTCACCTCCCCGCCCTTTCTTAGAGTG 1560
CAGTTCTTAGCCCTCTAGAAACGAGTTGGTGTCTTTTCGTCTCAGTAGCCCCCACCCTAAT 1620
AAGCTGTAGACATTGGTTTACAGTGAAACTATGCTATTCTCAGCCCTTTGAAACTCTGCT 1680
30 TCTCCTCCAGGGCCCGATTCCCAAACCCCATGGCTTCCCTCACACTGTCTTTTCTACCAT 1740
TTTCATTATAGAATGCTTCCAATCTTTTGTGAATTTTTTATTATAAAAAATCTATTTGTA 1800
TCTATCCTAACCAGTTTCGGGGATATATTAAGATATTTTTTGTACATAAGAGAGAAAGAGAG 1860
AGAAAAATTTATAGAAGTTTGTACAAATGGTTTAAATGTGTATATCTTGATACTTTAA 1920
CATGTAATGCTATTACCTCTGCATATTTTAGATGTGTAGTTCACCTTACAAGTCAATTT 1980
35 TCCCTATGTGGTTTTGTAAAGAACTCTCCTCATAGGTGAGATCAAGAGGCCACCAGTTGT 2040
ACTTCAGCACCAATGTGTCTTACTTTATAGAAATGTTGTTAATGTATTAATGATGTTATT 2100
AAATACTGTTCAAGAAGAACAAAGTTTATGCAGCTACTGTCCAACTCAAAGTGGCAGCC 2160
AGTTGGTTTTGATAGGTTGCCTTTTGGAGATTTCTATTACTGCCTTTTTTTTCTTACTGT 2220

TTTATTACAAACTTACAAAAATATGTATAACCCTGTTTTATACAAACTAGTTTCGTAATA 2280
AAACTTTTTCCTTTTTTTTAAAATG 2304

SEQ ID NO: 6

	Met	Glu	Ser	Ser	Ala	Lys	Met	Glu	Ser	Gly	10
5	Gly	Ala	Gly	Gln	Gln	Pro	Gln	Pro	Gln	Pro	20
	Gln	Gln	Pro	Phe	Leu	Pro	Pro	Ala	Ala	Cys	30
	Phe	Phe	Ala	Thr	Ala	Ala	Ala	Ala	Ala	Ala	40
	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Gln	Ser	Ala	50
	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	60
10	Gln	Gln	Ala	Pro	Gln	Leu	Arg	Pro	Ala	Ala	70
	Asp	Gly	Gln	Pro	Ser	Gly	Gly	Gly	His	Lys	80
	Ser	Ala	Pro	Lys	Gln	Val	Lys	Arg	Gln	Arg	90
	Ser	Ser	Ser	Pro	Glu	Leu	Met	Arg	Cys	Lys	100
	Arg	Arg	Leu	Asn	Phe	Ser	Gly	Phe	Gly	Tyr	110
15	Ser	Leu	Pro	Gln	Gln	Gln	Leu	Leu	Asp	Glu	120
	His	Asp	Ala	Val	Ser	Ala	Ala	Phe	Gln	Ala	130
	Gly	Val	Leu	Ser	Pro	Thr	Ile	Ser	Pro	Asn	140
	Tyr	Ser	Asn	Asp	Leu	Asn	Ser	Met	Ala	Gly	150
	Ser	Pro	Val	Ser	Ser	Tyr	Ser	Ser	Asp	Glu	160
20	Gly	Ser	Tyr	Asp	Pro	Leu	Ser	Pro	Glu	Glu	170
	Gln	Glu	Leu	Leu	Asp	Phe	Thr	Asn	Trp	Phe	180